



Supplementary Figure 1. Empirical P-values of the F_{ST} and XP-EHH analyses for all non-Asian populations using YRI as background within a +15kb region around rs368234815.

●/◆ denotes F_{ST} and XP-EHH for rs368234815 respectively; ●/◆ denotes F_{ST} and XP-EHH for all other variants in the region. All XP-EHH values are connected by a fitting curve (yellow line). The 1% tail of the genomic empirical distribution is indicated by the horizontal, dashed line.